On page 1, after the title, please insert the following section headings.

BACKGROUND OF THE INVENTION

1. Field of the Invention

On page 1, after the first complete paragraph, please insert the following section heading.

2. Description of the Related Art

On page 3, after the fourth complete paragraph, please insert the following section heading.

SUMMARY OF THE INVENTION

Please delete the paragraph bridging pages 4 and 5 and insert the following replacement paragraph:

A'

The homology or "degree of similarity" is used to denote nucleotide sequences which when aligned have similar (identical or conservatively replaced) nucleotides in like positions or regions. For example, two nucleotide sequences with at least 85% homology to each other have at least 85% homologous (identical or conservatively replaced nucleotides) in a like position when aligned optimally allowing for up to 3 gaps, with the provision that in respect of the gaps a total of not more than 15 amino acid residues is affected. The degree of similarity may be determined using methods well known in the art (see, for example, Wilbur, W.J. and Lipman, D.J. "Rapid Similarity Searches of Nucleic Acid and Protein Data Banks." Proceedings of the National Academy of Sciences USA 80, 726-730 (1983) and Myers E. and Miller W. "Optimal Alignments in Linear Space". Comput. Appl. Biosci. 4:11-17(1988)). One programme which may be used in determining the degree of similarity is the MegAlign Lipman-Pearson one pair method (using default parameters) which can be obtained from

A1 cont'd

DNAstar Inc, 1228, Selfpark Street, Madison, Wisconsin, 53715, USA as part of the Lasergene system. The test for homology of the sequence is based on the percent identity which is calculated by Fast DB based on the following parameters: mismatch penalty 1.0, gap penalty (1.00), gap size penalty 0.33 and joining penalty 30.0.

After the paragraph bridging pages 4 and 5, please insert the following section headings and specification paragraph:

BRIEF DESCRIPTION OF THE DRAWINGS

A2

Fig. 1 is a diagrammatic representation of the genomic organization of Beet Necrotic Yellow Vein Virus;

Fig. 2 is a diagram of the physical maps of pVDH239 and pVDH240;

Fig. 3 is a depiction of Southern blot analysis of T-DNA insertions into the genome of the primary sugar beet transformant T157-01;

Fig. 4 is a diagram of the individual ELISA values of the root extracts of various populations of sugar beet plants;

Fig. 5A is a graph of Rhizomania resistance of T157-01 F1; and

Fig. 5B is a depiction of Southern blot analysis of T-DNA insertions into the genome of the F1 progeny plants of T157-01.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

On page 10, please delete the last complete paragraph, and insert the following replacement paragraph:

A3

Figure 4 shows diagrams of the individual ELISA values of the root extracts of sugar beet plants of the populations Cadyx (susceptible control), Rifle (rhizomania tolerant variety), Rhizor (rhizomania tolerant variety) and T157-01 (GUS-positive F1 individuals) after inoculation with BNYVV-infested soil. Each number at the horizontal axis represents an individual plant.